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REMARKS

A. Status of the Claims

The Action indicates that claims 1 (a,b,d,e), 4 (a-o), 5-7, 10-12, 17 (SEQ ID NOs:18, 19), 24, and 37 drawn to SEQ ID NO:1 or encoding SEQ ID NO:2 are under consideration. Claims 1 and 4 are amended herein without prejudice or disclaimer and claims 39-40 added. Support for the amendments and new claims is found, at least, in original claim 4. Applicants reserve the right to pursue canceled material in subsequent prosecution.

B. Rejection Under 35 U.S.C. §112, Second Paragraph

The Action rejects claims 1, 4-7, 10-12, 24, and 37 for reciting "phytol kinase polypeptide," which is said to be unclear regarding whether the polypeptide is a complete phytol kinase. In response, Applicants note that the current claims do not recite this term. The rejection is therefore believed moot and removal thereof is thus respectfully requested.

C. Rejection Under 35 U.S.C. §112, First Paragraph—Written Description

The Action rejects the claims as encompassing subject matter not adequately described in the specification. In particular, it is asserted that claims directed to variants with less than 100% identity to SEQ ID NO:1 or encoding polypeptides with less than 100% identity to SEQ ID NO:2 are not adequately described.

In response, Applicants initially note that the current claims are directed to nucleic acids that encode a polypeptide having phytol kinase activity comprising an amino acid sequence with at least about 99% identity to the amino acid sequence of SEQ ID NO:2 or comprising at least 99% identity to SEQ ID NO:1. A written description of this subject matter is fully supported by the disclosure of SEQ ID NOs:1 and 2 in the Sequence Listing alone, not to mention the further detailed descriptions in the specification.

For example, the specification explains that SEQ ID NOs: 2, 6, and 37-68 of the Sequence listing represent plant phytol kinase polypeptides and that SEQ ID NOs: 20-27, 29-34, and 79 represent cyanobacterial phytol kinases. These sequences provide a description of the structural characteristics of phytol kinases generally, and in particular provide the conserved polypeptide sequences associated with phytol kinase activity.

In addition, written description must be reviewed from the perspective of one of skill in the art at the time the application is filed. *Wang Labs., Inc. v. Toshiba Corp.*, 993 F.2d 858, 863 (Fed. Cir. 1993). It was routine in the art as of the filing date to make silent changes to a given polypeptide while retaining activity. For example, changes can be made to coding sequence without changing the polypeptide sequence by altering codon usage. It is known in this regard that conservative amino acid substitutions can be made by substitution with residues having like characteristics, including hydropathic index or hydrophilicity (see, *e.g.*, U.S. 4,554,101). For instance, it is known that the relative hydropathic character of amino acids contributes to the secondary structure of the resultant protein and thus interaction of the protein with molecules such as enzymes, substrates, receptors, DNA, antibodies, antigens, etc. Based on hydrophobicity and charge characteristics, each amino acid has been assigned a hydropathic index and these are given in the specification. Those amino acids sharing a similar score may be selected and substituted for one another based on the known hydropathic indices.

Values for assessing hydrophilicity have also been assigned and can be used for selecting an amino acid for substitution. It is also known that amino acid substitutions can be based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, etc. There is, therefore, no basis in law or science to limit

Applicants to any less than what is being claimed. Withdrawal of the rejection is thus respectfully requested.

D. Rejection Under 35 U.S.C. §112, First Paragraph—Enablement

Claims 4, 10-12, 24, and 37 were rejected under 35 U.S.C. §112, first paragraph on the basis that the specification allegedly does not enable the skilled artisan to make and use the invention commensurate in scope with the claims. Applicants respectfully traverse.

First, as explained above, the currently claimed invention relates to nucleic acids encoding polypeptides with at least 99% identity to SEQ ID NO:2 or comprising at least 99% identity to SEQ ID NO:1. Second, the Action already acknowledges that the specification is enabled for a nucleic acid sequence of SEQ ID NO:1 and a nucleic acid encoding SEQ ID NO:2. It is respectfully submitted that this scope of subject matter acknowledged to be enabled alone demonstrates enablement for the entire scope of the claimed invention. It is well settled that Applicants need not provide working examples for each and every embodiment of the claims. *In re Buchner*, 929 F.2d 660, 661, 18 U.S.P.Q.2d 1331, 1332 (Fed. Cir. 1991); *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1384, 231 U.S.P.Q. 81, 94 (Fed. Cir. 1986), *cert. denied*, 480 U.S. 947 (1987); and *Lindemann Maschinenfabrik GMBC v. American Hoist & Derrick Co.*, 730 F.2d 1452, 1463, 221 U.S.P.Q. 481, 489 (Fed. Cir. 1984)). In addition, the scope of the enablement must only bear a "reasonable correlation" to the scope of the claims. *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970).

In the current case, at most routine experimentation would be required to make derivatives of SEQ ID NO:1 or SEQ ID NO:2 within the scope of the claims. Any such modifications would be guided by the nucleic acid and polypeptide sequences corresponding to phytol kinases provided in the specification. For example, as explained above, the sequences of

numerous plant and cyanobacterial phytol kinases are provided in the Sequence Listing. These sequences serve to demonstrate the regions associated with phytol kinase enzyme activity and therefore could be used to guide any modifications of the sequences provided.

As further explained above, it was routine as of the filing date to create sequence variants comprising silent nucleic acid mutations or those leading to conservative amino acid changes such that the activity of the encoded polypeptide is maintained. Creation of sequence variants would require only routine substitution of the starting nucleic acid molecules given the teaching in the specification. For example, it is known that conservative amino acid substitutions can be made by substitution of a residue with another having like characteristics. One criteria that may be used in this regard is the hydropathic index of amino acids. The significance of the hydropathic amino acid index in conferring biological function of a protein has been discussed by Kyte and Doolittle (*J. Mol.Biol.*, 157: 105-132, 1982). It is known that the relative hydropathic character of amino acids contributes to the secondary structure of the resultant protein and thus interaction of the protein with molecules such as enzymes, substrates, receptors, DNA, antibodies, antigens, etc. Based on hydrophobicity and charge characteristics, each amino acid has been assigned a hydropathic index and those amino acids sharing a similar score can be selected and substituted for one another based on the known hydropathic indices.

The specification therefore fully enables the claim scope based on the provision of SEQ ID NO:1 or SEQ ID NO:2 and other representative phytol kinases. While some mutagenesis would be required to generate sequence variants, this would not be undue in view of the teaching in the specification and knowledge in the art. The biological activity of any given sequence generated can routinely be confirmed by the transformation of plants with plant transformation

vectors comprising the sequences followed by measurement of activity using the same methodology described in the working examples.

In conclusion, Applicants have affirmatively demonstrated enablement of the claims and no basis to doubt the enablement has been provided. Removal of the rejection is thus respectfully requested.

E. Rejection Under 35 U.S.C. §102

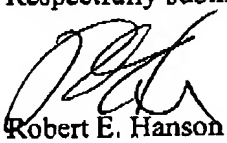
Claims 1, 4-7, 10-12, and 24 were rejected under 35 U.S.C. §102(b) as being anticipated by Alexandrov *et al.* (EP 1033405A2). In particular, the Action states that the reference discloses a sequence having 96.2% identity to SEQ ID NO:1 of the instant invention.

In response Applicants note that the current claims require nucleic acids having at least 99% identity to SEQ ID NO:1 or encoding a polypeptide with at least 99% identity to SEQ ID NO:2. This element is neither taught nor suggested by Alexandrov *et al.*, and is not asserted by the Action to do so. The rejection is therefore believed to be mot and removal of the rejection is thus respectfully requested.

CONCLUSION

The Examiner is invited to contact the undersigned attorneyat (512) 536-3085 with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,



Robert E. Hanson
Reg. No. 42,628
Attorney for Applicants

FULBRIGHT & JAWORSKI L.L.P.
600 Congress Avenue, Suite 2400
Austin, Texas 78701
(512) 474-5201

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